SEQUENCE LISTING

<110> Fritig, Bernard
Toquin, Valerie
Geoffroy, Pierrette
Legrand, Michel
Kauffmann, Serge

<120> INDUCIBLE COMTII PROMOTER, CHIMERA GENE CONTAINING SAME AND TRANSFORMED PLANTS

<130> A34638-PCT-USA

<140> US 09/937,204
<141> 2000-03-22

<150> PCT/FR99/03700
<151> 1999-03-22

<150> PCT/FR99/07646
<151> 1999-06-11

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cgt aac tgc aca tat gcc atg caa cta ttg tca tct tca gtc ctc ccc   96
Arg Asn Cys Thr Tyr Ala Met Gln Leu Leu Ser Ser Ser Val Leu Pro
            20                  25                  30

ttt gtg ttg cat tca aca att caa ttg gaa gtt ttt gag ata tta gcc   144
Phe Val Leu His Ser Thr Ile Gln Leu Glu Val Phe Glu Ile Leu Ala
        35                  40                  45

aaa tct aat gac act aaa ctt tct gct tct caa att gtt tct caa att   192
Lys Ser Asn Asp Thr Lys Leu Ser Ala Ser Gln Ile Val Ser Gln Ile
    50                  55                  60

cct aac tgc aca aaa cct gaa gca cct act atg tta aat agg atg ctt   240
Pro Asn Cys Thr Lys Pro Glu Ala Pro Thr Met Leu Asn Arg Met Leu
65                  70                  75                  80

tat gtc ttg gct agt tac tcc ttg ttt act tgt tcc att gtt gaa gat   288
Tyr Val Leu Ala Ser Tyr Ser Leu Phe Thr Cys Ser Ile Val Glu Asp
                85                  90                  95

gaa aaa aat aat ggg ggc caa aaa aga gtg tat ggt ttg tca caa gtg   336
Glu Lys Asn Asn Gly Gly Gln Lys Arg Val Tyr Gly Leu Ser Gln Val
            100                 105                 110

gga aaa ttc ttt gtt aaa aat gaa aat ggt gca tca atg ggg cca ctt   384
Gly Lys Phe Phe Val Lys Asn Glu Asn Gly Ala Ser Met Gly Pro Leu
        115                 120                 125

ttg gct ttg ctt caa aat aaa gta ttc ata aac agc tgg ttt gaa cta   432
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Leu Ala Leu Leu Gln Asn Lys Val Phe Ile Asn Ser Trp Phe Glu Leu
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Lys Asp Ala Val Leu Glu Gly Gly Val Pro Phe Asp Arg Val His Gly
145                 150                 155                 160

gtg cat gca ttt gaa tat cca aaa tcg gac cca aaa ttc aat gat gtt   528
Val His Ala Phe Glu Tyr Pro Lys Ser Asp Pro Lys Phe Asn Asp Val
                165                 170                 175

ttc aac aag gca atg atc aat cac aca act gta gtc atg aaa aaa ata   576
Phe Asn Lys Ala Met Ile Asn His Thr Thr Val Val Met Lys Lys Ile
            180                 185                 190

ctt gaa aat tac aaa ggt ttt gag aac ctt aaa act ttg gtt gat gtt   624
Leu Glu Asn Tyr Lys Gly Phe Glu Asn Leu Lys Thr Leu Val Asp Val
        195                 200                 205

gga ggt ggt ctt gga gtt aac ctc aag atg att aca tct aaa tac ccc   672
Gly Gly Gly Leu Gly Val Asn Leu Lys Met Ile Thr Ser Lys Tyr Pro
    210                 215                 220

aca att aag ggc act aat ttt gat ttg cca cat gtt gtt caa cat gcc   720
Thr Ile Lys Gly Thr Asn Phe Asp Leu Pro His Val Val Gln His Ala
225                 230                 235                 240

cct tcc tat cct ggg gtg gaa cat gtt ggg gga gat atg ttt gaa agt   768
Pro Ser Tyr Pro Gly Val Glu His Val Gly Gly Asp Met Phe Glu Ser
                245                 250                 255

gtt cca gaa gga gat gct att ttt atg aag tgg att ctt cat gac tgg   816
Val Pro Glu Gly Asp Ala Ile Phe Met Lys Trp Ile Leu His Asp Trp
            260                 265                 270

agt gat agt cac aac ctc aag ttg cta aag aac tgc tac aag gct cta   864
Ser Asp Ser His Asn Leu Lys Leu Leu Lys Asn Cys Tyr Lys Ala Leu
        275                 280                 285

cca gac aat gga aag gtg att gtt gtt gag gcc att tta cca gtg aaa   912
Pro Asp Asn Gly Lys Val Ile Val Val Glu Ala Ile Leu Pro Val Lys
    290                 295                 300

cca gac att gac acc gca gtg gtt ggc gtt tcg caa tgt gat ttg atc   960
Pro Asp Ile Asp Thr Ala Val Val Gly Val Ser Gln Cys Asp Leu Ile
305                 310                 315                 320

atg atg gct caa aat cct gga ggc aaa gag cga tcg gaa gag gag ttt  1008
Met Met Ala Gln Asn Pro Gly Gly Lys Glu Arg Ser Glu Glu Glu Phe
                325                 330                 335

cga gcc ttg gct act gaa gct gga ttc aaa ggc gtt aac tta ata tgt  1056
Arg Ala Leu Ala Thr Glu Ala Gly Phe Lys Gly Val Asn Leu Ile Cys
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tgt gtc tgt aat ttt tgg gtc atg gaa ttc tgc aag tag              1095
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1 5 10 15

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Ser Ala Asn Ala Thr Ala Cys Thr Ala Thr Gln Gln Thr Ala Ala Tyr
20 25 30

aag aca ctc gtg agc atc ctg tcg gac gcg tcg ttc aac aag tgc tct 144

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Lys Thr Leu Val Ser Ile Leu Ser Asp Ala Ser Phe Asn Lys Cys Ser
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Thr Asp Ser Gly Tyr Ser Met Leu Thr Ala Lys Ala Leu Pro Thr Thr
     50                  55                  60

gcg cag tac aag ctc atg tgc gcg tcc acg gca tgc aac acc atg atc   240
Ala Gln Tyr Lys Leu Met Cys Ala Ser Thr Ala Cys Asn Thr Met Ile
 65                  70                  75                  80

aag aag atc gtg acg ctg aac ccg ccc aac tgc gac ctg acg gtg ccc   288
Lys Lys Ile Val Thr Leu Asn Pro Pro Asn Cys Asp Leu Thr Val Pro
                 85                  90                  95

acg agc ggc ctg gtg ctc aac gtg tac tcg tac gcg aac ggc ttc tcg   336
Thr Ser Gly Leu Val Leu Asn Val Tyr Ser Tyr Ala Asn Gly Phe Ser
            100                 105                 110

gac aag tgc tcg tcg ctg                                          354
Asp Lys Cys Ser Ser Leu
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<213> Phytophthora megasperma

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agc atc ctg tcg gac gcg tcg ttc aac aag tgc tct acg gat tcg ggc   96
Ser Ile Leu Ser Asp Ala Ser Phe Asn Lys Cys Ser Thr Asp Ser Gly
            20                  25                  30

tac tcc atg ctg acg gcc aag gcc ctc ccc acc acg gcg cag tac aag   144
Tyr Ser Met Leu Thr Ala Lys Ala Leu Pro Thr Thr Ala Gln Tyr Lys
        35                  40                  45

ctc atg tgc gcg tcc acg gca tgc aac acc atg atc aag aag atc gtg   192
Leu Met Cys Ala Ser Thr Ala Cys Asn Thr Met Ile Lys Lys Ile Val
    50                  55                  60

acg ctg aac ccg ccc aac tgc gac ctg acg gtg ccc acg agc ggc ctg   240
Thr Leu Asn Pro Pro Asn Cys Asp Leu Thr Val Pro Thr Ser Gly Leu
65                  70                  75                  80

gtg ctc aac gtg tac tcg tac gcg aac ggc ttc tcg gac aag tgc tcg   288
Val Leu Asn Val Tyr Ser Tyr Ala Asn Gly Phe Ser Asp Lys Cys Ser
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acc atg aac ttc acc gct ctg ctc gct gcc gtc gcc gcc gcc ttg gtc   1308
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     1               5                  10                  15

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Gly Ser Ala Asn Ala Thr Ala Cys Thr Ala Thr Gln Gln Thr Ala Ala
                20                  25                  30

tac aaa aca ctc gtg agc atc ctg tcg gac gcg tcg ttc aac aag tgc   1404
Tyr Lys Thr Leu Val Ser Ile Leu Ser Asp Ala Ser Phe Asn Lys Cys
            35                  40                  45

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acg gcg cag tac aag ctc atg tgc gcg tcc acg gca tgc aac acc atg   1500
Thr Ala Gln Tyr Lys Leu Met Cys Ala Ser Thr Ala Cys Asn Thr Met
     65                  70                  75

atc aaa aaa atc gtg acg ctg aac ccg ccc aac tgc aac ctg acg gtg   1548
Ile Lys Lys Ile Val Thr Leu Asn Pro Pro Asn Cys Asn Leu Thr Val
 80                  85                  90                  95

ccc acg agc ggc ctg gtg ctc aac gtg tac tcg tac cca aac ggc ttc   1596
Pro Thr Ser Gly Leu Val Leu Asn Val Tyr Ser Tyr Pro Asn Gly Phe
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Ser Asp Lys Cys Ser Ser Leu  *
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<210> 25
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US 099372040AP1

Creation date: 04-08-2003
Indexing Officer: HTON1 - HUAN TON
Team: OIPEBackFileIndexing
Dossier: 09937204

Legal Date: 11-02-2003

No.	Doccode	Number of pages
1	M903	2

Total number of pages: 2

Remarks:

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